GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: January 28, 2006, 08:01:18 ; Search time 545 Seconds
(without alignments)
5188.245 Million cell updates/sec

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Perfect score: 3404
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6059551 seqs, 415333918 residues

Total number of hits satisfying chosen parameters: 12119102

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 22	2391.6	70.3	3819	8	US-11-009-873A-243	Sequence 243, App
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;  TYPE: DNA
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;  FEATURE:
;  OTHER INFORMATION: bacterial cloning vector
US-11-045-468A-18

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GENERAL INFORMATION:
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;  APPLICANT: Ng, Patrick
;  APPLICANT: Wei, Chialin
;  APPLICANT: Ruan, Yijun
;  TITLE OF INVENTION: Method for Gene Identification Signature (GIS) Analysis
;  FILE REFERENCE: 3240-107
;  CURRENT APPLICATION NUMBER: US/11/045,468A
;  CURRENT FILING DATE: 2005-01-31
;  PRIOR APPLICATION NUMBER: 10/664,234
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;  Publication No. US20050255501A1
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                    Copyright (c) 1993 - 2006  Bioacceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

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	4	2699.2	79.3	2743	9	US-10-903-632-660	Sequence 660, App
c	5	2690.8	79.0	4283	7	US-10-374-853-1	Sequence 1, Appli
	6	2639.2	77.5	4082	7	US-10-363-082-3	Sequence 3, Appl
	7	2639.2	77.5	7387	3	US-09-867-947-28	Sequence 28, Appl
	8	2639.2	77.5	8618	8	US-09-744-558-5	Sequence 5, Appl
	9	2636.4	77.5	12225	7	US-10-646-628-1	Sequence 7, Appl
c	10	2634.6	77.4	4201	3	US-10-792-568-7	Sequence 1, Appl
	11	2634.6	77.4	4928	7	US-10-420-529-10	Sequence 10, Appl
	12	2634	77.4	10600	7	US-10-356-708-1	Sequence 1, Appli
	13	2634	77.4	10600	7	US-10-280-913A-1	Sequence 1, Appli
	14	2634	77.4	10600	7	US-10-684-134-1	Sequence 1, Appli
	15	2634	77.4	10600	8	US-10-637-758-1	Sequence 1, Appli
	16	2634	77.4	10624	6	US-10-356-708-2	Sequence 2, Appli
	17	2634	77.4	10624	7	US-10-280-913A-2	Sequence 2, Appli
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	25	2633.6	77.4	4960	6	US-10-014-099F-13	Sequence 13, Appl
	26	2633.6	77.4	5290	6	US-10-014-099F-76	Sequence 76, Appl
	27	2633.6	77.4	5309	6	US-10-014-099F-77	Sequence 77, Appl
	28	2632.6	77.4	5430	9	US-10-685-837-16	Sequence 16, Appl
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	31	2633.6	77.4	5730	6	US-10-014-099F-73	Sequence 73, Appl
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	38	2632.6	77.3	4346	8	US-11-161-408-26	Sequence 113, App
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;   NAME/KEY: misc_feature
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;   OTHER INFORMATION: region from 15 to 704 represents the stuffer fragment, comprising
;   OTHER INFORMATION: MmeI and BamHI, that is removed during cloning
US-10-664-234-18
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Qy  181  CATGAAGGTGAAAATTAAAATGTTGGAATGGTGTGGCGCTCGTTAGCTCATGA         240
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: January 28, 2006, 07:24:12 ; Search time 577 Seconds
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Scoring table: IDENTITY NUC
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Searched: 1303057 seqs, 88878028 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                 Listing first 150 summaries

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Issued_Patents NA:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	2690.8	79.0	4283	3	US-09-614-178-1	Sequence 1, Appli
5	2639.2	79.5	7387	3	US-09-238-356-28	Sequence 28, Appli
6	2637.2	77.5	8854	3	US-09-053-549-1	Sequence 1, Appli
7	2634.0	77.4	4201	3	US-09-792-568-7	Sequence 7, Appli
8	2628.6	77.2	5767	3	US-09-810-861B-3	Sequence 3, Appli
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RESULT 1

US-08-343-401A-3

Sequence 3, Application US/08343401A

Patent No. 561132

GENERAL INFORMATION:

APPLICANT: Swain, William F
APPLICANT: Macklin, Michael D
APPLICANT: Eriksson, Elof
APPLICANT: Andree, Christophe

TITLE OF INVENTION: Improved Wound Healing

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: PO Box 2113
CITY: Madison

STATE: WI
COUNTRY: USA
ZIP: 53701-2113

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,401A
FILING DATE: 22-NOV-1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9103-9

TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
TELEX: 608-251-9166

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4283 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)

IMMEDIATE SOURCE:
CLONE: pWRG1630

FEATURE:
NAME/KEY: exon
LOCATION: 713..721

FEATURE:
NAME/KEY: exon
LOCATION: 981..1253

FEATURE:
NAME/KEY: CDS
LOCATION: join(713..721, 981..1253)

FEATURE:
NAME/KEY: sig_peptide
LOCATION: 713..1049

US-08-343-401A-3

Query Match   79.0%; Score 2690.8; DB 2; Length 4283;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 2692; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.7
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c	72	851.6	25.0	858	11	DE097419	DE097419 Oryzias 1
c	73	851.6	25.0	859	11	DE097698	DE097698 Oryzias 1
c	74	851.6	25.0	861	11	DE097365	DE097365 Oryzias 1
c	75	850.6	25.0	860	11	DE097386	DE097386 Oryzias 1
c	76	850.6	25.0	860	11	DE097406	DE097406 Oryzias 1
c	77	850.6	25.0	860	11	DE100231	DE100231 Oryzias 1
c	78	850.6	25.0	860	11	DE102247	DE102247 Oryzias 1
c	79	850.6	25.0	860	11	DE105059	DE105059 Oryzias 1
c	80	850.4	25.0	875	8	CX012952	CX012952 io62d12.b
c	81	850	25.0	860	11	DE097689	DE097689 Oryzias 1
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c	83	847.6	24.9	857	11	DE096885	DE096885 Oryzias 1
c	84	847.6	24.9	858	11	DE097532	DE097532 Oryzias 1
c	85	847	24.9	858	11	DE096898	DE096898 Oryzias 1
c	86	846.6	24.9	854	11	DE100230	DE100230 Oryzias 1
c	87	846.6	24.9	854	11	DE102262	DE102262 Oryzias 1
c	88	846.6	24.9	856	11	DE096624	DE096624 Oryzias 1
c	89	845.6	24.8	867	11	DE097026	DE097026 Oryzias 1
c	90	844.6	24.8	852	11	DE097385	DE097385 Oryzias 1
c	91	844.6	24.8	854	11	DE096642	DE096642 Oryzias 1
c	92	844.6	24.8	854	11	DE096808	DE096808 Oryzias 1
c	93	844.6	24.8	854	11	DE096883	DE096883 Oryzias 1
c	94	844.6	24.8	854	11	DE100114	DE100114 Oryzias 1
c	95	843.6	24.8	853	11	DE097361	DE097361 Oryzias 1

c	#					Accession	Organism	Accession	Organism
c	96	843.6	24.8	853	11	DE097512	Oryzias 1	DE097512	Oryzias 1
c	97	843.6	24.8	853	11	DE098633	Oryzias 1	DE098633	Oryzias 1
c	98	843.6	24.8	853	11	DE104282	Oryzias 1	DE104282	Oryzias 1
c	99	843.6	24.8	850	11	DE098928	Oryzias 1	DE098928	Oryzias 1
c	100	840.6	24.7	849	11	DE098584	Oryzias 1	DE098584	Oryzias 1
c	101	839.4	24.7	841	1	AL042026	DKFZp434E	AL042026	DKFZp434E
c	102	838.6	24.6	1269	10	AG393068	Mus muscu	AG393068	Mus muscu
c	103	835.8	24.6	853	11	DE098497	Oryzias 1	DE098497	Oryzias 1
c	104	835.6	24.5	843	11	DE099850	Oryzias 1	DE099850	Oryzias 1
c	105	835.6	24.5	845	11	DE097432	Oryzias 1	DE097432	Oryzias 1
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c	108	830.6	24.4	840	11	DE096674	Oryzias 1	DE096674	Oryzias 1
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c	112	829.6	24.4	839	11	DE100578	Oryzias 1	DE100578	Oryzias 1
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c	114	828.6	24.3	838	11	DE104698	Oryzias 1	DE104698	Oryzias 1
c	115	828.6	24.3	838	11	DE097036	Oryzias 1	DE097036	Oryzias 1
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c	120	824.6	24.3	834	11	BM438950	IplvrC0049	BM438950	IplvrC0049
c	121	823	24.2	854	3	DE096859	Oryzias 1	DE096859	Oryzias 1
c	122	819.6	24.1	841	11	CV984340	UMC-bov_0	CV984340	UMC-bov_0
c	123	819.6	24.1	868	11	AG332951	Mus muscu	AG332951	Mus muscu
c	124	818.8	24.1	1169	10	DE098943	Oryzias 1	DE098943	Oryzias 1
c	125	818.6	24.0	828	11	DE102303	Oryzias 1	DE102303	Oryzias 1
c	126	818.6	24.0	828	11	DE097651	Oryzias 1	DE097651	Oryzias 1
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c	132	815.2	23.9	841	8	DE096622	Oryzias 1	DE096622	Oryzias 1
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c	134	814.8	23.9	1249	9	DE096853	Oryzias 1	DE096853	Oryzias 1
c	135	814.6	23.9	825	11	DR046031	FP-8_F02.	DR046031	FP-8_F02.
c	136	813	23.9	1195	9	BZ577702	msh2_5533	BZ577702	msh2_5533
c	137	812.8	23.9	1126	9	DE099603	Oryzias 1	DE099603	Oryzias 1
c	138	812.8	23.9	822	11	CX013029	io62h07.b	CX013029	io62h07.b
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c	144	807.8	23.7	856	7	DE098338	Oryzias 1	DE098338	Oryzias 1
c	145	807.6	23.7	817	11	DE098459	Oryzias 1	DE098459	Oryzias 1
c	146	807.6	23.7	817	11	DE103919	Oryzias 1	DE103919	Oryzias 1
c	147	807.6	23.7	817	11	DE099494	Oryzias 1	DE099494	Oryzias 1
c	148	806.6	23.7	816	11	DE099569	Oryzias 1	DE099569	Oryzias 1
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c	150	806.6	23.7	1321	10				

RESULT 1
AJ281552
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DEFINITION Anopheles gambiae 4A3A-P6F11-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P6F11, mRNA sequence.
ACCESSION   AJ281552
VERSION   AJ281552.1   GI:6922432
KEYWORDS   EST.
SOURCE   Anopheles gambiae (African malaria mosquito)
  ORGANISM Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Culicidae; Anophelinae; Anopheles.
REFERENCE   1 (bases 1 to 1070)
  AUTHORS   Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
            Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
            and Kafatos,F.C.
  TITLE   Anopheles gambiae pilot gene discovery project: identification of
            mosquito innate immunity genes from expressed sequence tags
            generated from immune-competent cell lines
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
  PUBMED   10841561
COMMENT   Contact: Dimopoulos G
            Fotis C. Kafatos Laboratory
            European Molecular Biology Laboratory
            Meyerhofstrasse 1, 69117 Heidelberg, Germany.
FEATURES   Location/Qualifiers
     source   1..1070
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
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                     /cell_line="immune competent 4A3A"
                     /lab_host="E. coli DH10B"
                     /clone_lib="Anopheles gambiae immune competent 4A3A"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from
                     forward priming site which reads from the 3' end of the
                     cDNA. The 4A3A is a directionally cloned and normalized
                     cDNA library that was constructed from the 4A3A cell line
                     oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
                     (1996). Normalization and Subtraction: Two approaches To
                     Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN

Query Match   30.9%; Score 1051; DB 1; Length 1070;
Best Local Similarity   99.4%;
Matches 1065; Conservative   0; Mismatches   5; Indels   1; Gaps   1;

                        Pred. No. 4.9e-293;

ALIGNMENTS

Qy   1156 TTGCTGGCCGTTTTTCGATAGAGGCTCCGCGCCCCCCCTGACGAGCAGCATCACAAAAATCGACGGCTCA 1215
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Db   1 TTGCTGGCCGTTTTTCGATAGAGGCTCCGCGCCCCCCCTGACGAGCAGCATCACAAAAATCGACGGCTCA 60

Qy   1216 AGTCAGAGGTGGCGAAAACCCGACACAGACTATAAAAGATACCAGGCGGTTTCCCCCTGGAAGC 1275
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Db   61 AGTCAGAGGTGGCGAAAACCCGACACAGACTATAAAAGATACCAGGCGGTTTCCCCCTGGAAGC 120

Qy   1276 TCCCCTGGTGCGCGGCTCTCCCTGTACCGGACCCCTGCGGCGGTTACCGGGATACCGGTCCGGCCCTTTCTC 1335
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCCCCTGGTGCGCGGCTCTCCCTGTACCGGACCCCTGCGGCGGTTACCGGGATACCGGTCCGGCCCTTTCTC 180

Qy   1336 CCTTCGGGAAGGCGTGGCGGCCTTTCTCATAGCTCACGCGCTGTAGGTATCTCAGTTCGGGTGTAG 1395
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Qy   1396 GTCGGTTCGGCTCCAAGCTGGGGCTGTGGTGCACAGAACCCCCGGTTCAGCCGACCGGGCGCC 1455
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Qy   1636 AAGCCAGTTACCTTCGGAAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAAACCACCGCT 1695
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Db   481 AAGCCAGTTACCTTCGGAAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAAACCACCGCT 540

OM nucleic - nucleic search, using sw model

Run on: January 28, 2006, 06:39:27 ; Search time 1926 Seconds
                                             (without alignments)
                                             11779.135 Million cell updates/sec

Title: US-10-664-234-18
Perfect score: 3404
Sequence: 1 gggcggaattctcgagcggccc.........ttgtaatacgactcactata 3404

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :
  1: N_Geneseq_21:*
  2: geneseqp1980s:*
  3: geneseqp1990s:*
  4: geneseqn2000s:*
  5: geneseqn2001s:*
  6: geneseqn2001bs:*
  7: geneseqn2002as:*
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  9: geneseqn2003as:*
 10: geneseqn2003bs:*
 11: geneseqn2003cs:*
 12: geneseqn2003ds:*
 13: geneseqn2004as:*
 14: geneseqn2004bs:*
 15: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3404	100.0	3404	14	ADY71944	Ady71944 Vector pG
c	2	2699.2	79.3	2739	14	ADZ78428	Adz78428 Alpha-fra
c	3	2699.2	79.3	2739	14	ADZ78427	Adz78427 Alpha-fra
c	4	2699.2	79.3	2743	14	ADZ78426	Adz78426 Alpha-fra
	5	2690.8	79.0	4283	2	AAT86449	Aat86449 DNA encod
	6	2690.8	79.0	4283	2	AAT86610	Aat86610 Epidermal
	7	2690.8	79.0	4283	2	AAA63237	Aaa63237 Plasmid p
	8	2690.8	79.0	4283	9	ABX93095	Abx93095 DNA seque
	9	2690.8	79.0	4283	12	ADJ98301	Adj98301 Plasmid p
c	10	2677.2	78.6	8237	6	AAL45377	Aal45377 Recombina
c	11	2639.2	77.5	4082	6	AAD33877	Aad33877 pIW17 vec
c	12	2639.2	77.5	5143	13	ADT66834	Adt66834 MVA shutt
	13	2639.2	77.5	7173	14	ADY99889	Ady99889 Exemplary
c	14	2639.2	77.5	8618	12	ADQ91623	Adq91623 Plasmid p
c	15	2637.2	77.5	8854	2	AAZ20086	Aaz20086 DNA encod
c	16	2636.4	77.5	5326	13	ADT66833	Adt66833 MVA shutt
	17	2636.4	77.5	12225	6	AAD46400	Aad46400 pIW-48 pl
	18	2636.4	77.5	12225	10	ADR06532	Ade06532 Plasmid t
	19	2636.4	77.5	12225	13	ADT66779	Adt66779 Plasmid p
c	20	2634.6	77.4	4201	6	ABS53597	Abs53597 Noursecth
c	21	2634	77.4	10600	11	ADM68432	Adm68432 Celery CB
c	22	2634	77.4	10600	12	ADP26585	Adp26585 TMV CEL_I
c	23	2634	77.4	10600	13	ADQ88407	Adq88407 pl177MP4-
c	24	2634	77.4	10600	14	ADS17161	Ads17161 pl177 MP4
c	25	2634	77.4	10624	11	ADM68433	Adm68433 Celery CB
c	26	2634	77.4	10624	12	ADP26586	Adp26586 TMV CEL_I
c	27	2634	77.4	10624	13	ADQ88408	Adq88408 pl177MP4-
c	28	2634	77.4	11222	13	ADS17162	Ads17162 pl177 MP4
c	29	2634	77.4	11222	12	ADN97500	Adn97500 Artificia
c	30	3858	77.4	3858	5	AAD04947	Aad04947 Plasmid p
c	31	2633.6	77.4	4886	6	ABT08169	Abt08169 Recombina
c	32	2633.6	77.4	4905	6	ABT08170	Abt08170 Recombina
c	33	2633.6	77.4	4960	4	AAD09269	Aad09269 pCMV-I-Cr
c	34	2633.6	77.4	4960	6	ABT08148	Abt08148 Recombina
c	35	2633.6	77.4	5290	6	ABT08171	Abt08171 Recombina
c	36	2633.6	77.4	5309	6	ABT08172	Abt08172 Recombina
c	37	2633.6	77.4	5430	12	ADN11355	Adn11355 GAGGS-tet
c	38	2633.6	77.4	5711	6	ABT08145	Abt08145 Recombina
c	39	2633.6	77.4	5723	6	ABT08147	Abt08147 Recombina
c	40	2633.6	77.4	5741	10	ABT08168	Abt08168 Recombina
c	41	2633.6	77.4	5741	10	ADB81340	Adb81340 Codon opt
c	42	2633.6	77.4	5878	6	ABT08199	Abt08199 Recombina
c	43	2633.6	77.4	5878	12	ADN11357	Adn11357 CAGGS-cre
c	44	2633.6	77.4	6641	6	ABT08200	Abt08200 Recombina
c	45	2633.6	77.4	7332	4	AAD09270	Aad09270 pCMV-I-be
c	46	2633.6	77.4	7332	12	ADN11356	Adn11356 CMV-LacZ
c	47	2632.6	77.3	4346	8	ABT16615	Abt16615 Artificia
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c	53	2632.6	77.3	5410	13	ADT99436	Adt99436 Plant DNA
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	55	2632.6	77.3	8062	5	AAD04946	Aad04946 Plasmid p
	56	2632.6	77.3	8153	5	AAD04946	Aad04946 Plasmid p
	57	2632.6	77.3	8752	12	ADK51933	Adk51933 Novel rRN
c	58	2631	77.3	5711	5	AAD04935	Aad04935 C31-Int e
c	59	2631	77.3	2762	12	ADI36475	Adi36475 Plasmid B
	60	2631	77.3	2803	12	ADI36474	Adi36474 Plasmid A
	61	2630.8	77.3	6565	5	AAF55126	Aaf55126 Nucleotid
	62	2630.8	77.3	6971	5	AAF55124	Aaf55124 Nucleotid
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	64	2630.6	77.3	7969	5	AAF55123	Aaf55123 Nucleotid
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	69	2629	77.2	2686	12	ADH58310	Adh58310 DNA seque
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c	72	2628.6	77.2	6287	6	AAK98923	Aak98923 Human pMS
c	73	2628.6	77.2	6347	6	AAK98930	Aak98930 Human pMS
c	74	2628.6	77.2	9937	13	ADT04846	Adt04846 Vector DN
c	75	2628.6	77.2	15965	14	AEB17031	Aeb17031 Targeting
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	77	2627.6	77.2	6295	2	AAV02043	Aav02043 Plasmid p
	78	2627.6	77.2	7164	5	AAD10238	Aad10238 Commercia
	79	2627.6	77.2	7383	5	AAS00153	Aas00153 Matrix me
	80	2625.8	77.1	4045	5	AAQ70942	Aaq70942 Plasmid p
c	81	2625.8	77.1	5848	3	AAC55481	Aac55481 Destinati
c	82	2625.8	77.1	5897	2	AAV63741	Aav63741 Plasmid p
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	85	2625.4	77.1	4776	2	AAX77617	Aax77617 Expressio
c	86	2625.4	77.1	9335	12	AAV63734	Aav63734 Plasmid p
	87	2623.4	77.1	9639	12	ADG98662	Adg98662 Baculovir
	88	2623.4	77.1	9698	13	ADU47350	Adu47350 Vector A5
	89	2622.4	77.1	9780	2	AAV82817	Aave2817 Recombina
	90	2623.4	77.0	9698	2	ABT08149	Abt08149 Recombina
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RESULT 1

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AC   ADY71944;
XX
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XX
DE   Vector pGIS1.
XX
KW   cloning; mapping; ditag; vector; ss.
XX
OS   Synthetic.
XX
PN   US2005059022-A1.
XX
PD   17-MAR-2005.
XX
PF   17-SEP-2003; 2003US-00664234.
XX
PR   17-SEP-2003; 2003US-00664234.
XX
PA   (SCTE-) AGENCY SCI TECHNOLOGY & RES.
XX
PI   Ruan Y, Ng P, Wei C;
XX
DR   WPI; 2005-240897/25.
XX
PT   New isolated oligonucleotides comprising at least one ditag, useful for
PT   gene identification signature analysis or for gene discovery or genome
PT   mapping.
XX
PS   Claim 20; SEQ ID NO 18; 33pp; English.
XX
CC   The invention relates to an isolated oligonucleotide comprising at least
CC   one ditag, where the ditag includes 2 joined first and second sequence
CC   tags, where the first tag includes a 5'-terminus sequence and the second
CC   tag comprises the 3'-terminus sequence of a nucleic acid molecule or its
CC   fragment. The oligonucleotide further comprises two adapter sequence
CC   (preferably containing restriction enzyme sites) flanking the ditag. The
CC   composition and methods using it are useful for gene identification
CC   signature analysis, for gene discovery or genome mapping or for isolating
CC   full length cDNAs. These may also be used for measuring transcript
CC   abundance in transcriptomes, for annotating genome sequences or for
CC   enhancing sequencing efficiency. This sequence corresponds to the vector
CC   pGIS1 containing a ditag oligonucleotide sequence of the invention.
XX
SQ   Sequence 3404 BP; 812 A; 872 C; 894 G; 826 T; 0 U; 0 Other;
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Query Match   100.0%; Score 3404; DB 14; Length 3404;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

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95		2621.6	77.0	4950	8	Abx64322	Transdomi
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97		2621.6	77.0	4950	14	Add28942	Retrovira
98		2621.6	77.0	4950	14	Ady21075	Transdomi
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104		2621.6	77.0	6253	9	Aal57215	MIG retro
105		2621.6	77.0	6505	9	Ada12886	Murine MS
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118		2621.6	77.0	12022	2	Aax82260	Factor VI
119		2621.6	77.0	12200	14	Adv34803	Vector pA
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125		2620	77.0	4163	2	Aaq32349	Template
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128		2618.4	76.9	5421	2	Aac68299	SV40/APPA
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137		2617	76.9	6561	14	Aea04980	Retrovira
138		2617	76.9	7244	14	Aea04979	Retrovira
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147	c	2612	76.7	4949	10	Abx04119	Retrovira
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Qy     61 GGCTGGGCGGCTACTTCGGAGGAGCCCCGGACGCGGCGGCGTCGTTTTTTATACATTCCCGCGCCG    120
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Qy    121 GAGGCACGGAGGAGGCGGGGCGGGGCGCTCGTTGATTAGGCCGCGGGAGGTCACAGGCTC       180
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Qy    241 TGAGAACTGCGCGGCATCTGCAGGATGGGCGTTTAATGGGCTGCTGTCCAGAGTGTAAGGTGCC    300
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GenCore version 5.1.7
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Run on: January 28, 2006, 07:14:47 ; Search time 16857 Seconds
        (without alignments)
        11478.621 Million cell updates/sec

OM nucleic - nucleic search, using sw model

Title: US-10-664-234-18
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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172565 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 150 summaries

Database :   GenEmbl.*
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       14: gb_htg:*
       15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3404	100.0	3404	6	CS091374	CS091374 Sequence
2	2699.2	79.3	2743	11	X65304	X65304 Cloning vec
3	2690.8	79.0	4283	6	I63120	I63120 Sequence 3
4	2690.8	79.0	4283	6	I85496	I85496 Sequence 1
c 5	2679.8	78.7	10163	11	AY860671	AY860671 Expressio
c 6	2671.4	78.5	7528	11	AY608405	AY608405 Cysteine-
c 7	2650.6	77.9	4674	11	U02437	U02437 Cloning vec
c 8	2649.2	77.8	3394	11	AF062083	AF062083 Cloning v
c 9	2649.2	77.8	3394	11	AF083409	AF083409 Cloning v
c 10	2649.2	77.8	3604	11	AF062078	AF062078 Cloning v
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13	2649.2	77.8	3714	11	AF083408	AF083408 Cloning v
14	2649.2	77.8	3946	11	AF134573	AF134573 Cloning v
15	2649.2	77.8	4026	11	AF062080	AF062080 Cloning v
16	2649.2	77.8	4154	11	AF062082	AF062082 Cloning v
17	2649.2	77.8	4503	11	AF062081	AF062081 Cloning v
18	2649.2	77.8	4795	11	AF134572	AF134572 Cloning v
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22	2649.2	77.8	6023	6	AY652437	AY652437 Promoter-
23	2649.2	77.8	6664	11	AY652438	AY652438 Promoter-
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71	2628.6	77.2	11612	6	AR575401	AR575401 Sequence
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c	92	2626.6	77.2	23250	11	AY336796	AY336796	Transform
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c	144	2621.6	77.0	15528	11	A93016	A93016	Sequence 4
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c	150	2620.6	77.0	6089	11	EVPAN81	Z32751	Expression

ALIGNMENTS

RESULT 1
CS091374

LOCUS   CS091374   3404 bp   DNA   linear   PAT 03-JUN-2005
DEFINITION Sequence 18 from Patent EP1533386.
ACCESSION   CS091374
VERSION   CS091374.1 GI:66948703
KEYWORDS
SOURCE   synthetic construct
  ORGANISM synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Ruan,Y., Ng,P. and Wei,C.
  TITLE   Method for gene identification signature (GIS) analysis
  JOURNAL   Patent: EP 153386-A 18 25-MAY-2005;
            Agency for Science, Technology and Research (SG)
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence of pGIS1"
     misc_feature   15..704
                     /note="region from 15 to 704 represents the stuffer
                     fragment, comprising MmeI and BamHI, that is removed
                     during cloning"
ORIGIN

Query Match   100.0%; Score 3404; DB 6; Length 3404;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 3404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GGGCGGAATTCTCGAGCGCGGCCCGGACCGAGAGGGCCTTGCGCCGGCGT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCGGAATTCTCGAGCGCGGCCCGGACCGAGAGGGCCTTGCGCCGGCGT 60

Qy   61 GGCTGGGCGGCTACTTCGGAGGACCCCGACGCGCGGGTCGTTTTTATACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GGCTGGGCGGCTACTTCGGAGGACCCCGACGCGCGGGTCGTTTTTATACA 120

Qy   121 GAGGCAACGGAAGGGGCGGGGGGCCCTCGTGATTAGGCGGCGGGCTCGTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GAGGCAACGGAAGGGGCGGGGGGCCCTCGTGATTAGGCGGCGGGCTCGTT 180

Qy   181 CATGAAGGTGAAAATTAAATGTTGGAATGGTGGCGGCCACTTGGCTGAAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CATGAAGGTGAAAATTAAATGTTGGAATGGTGGCGGCCACTTGGCTGAAT 240

Qy   241 TGAGAACTGCGCGCATCTTGCAGGATGCCGTTTAATGGCGTGCGTCCAGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGAGAACTGCGCGCATCTTGCAGGATGCCGTTTAATGGCGTGCGTCCAGA 300

Qy   301 TGGTGATGACTGCCCCCTGTGTGGGGACAGTGCTCCCACTGCACATGCAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGGTGATGACTGCCCCCTGTGTGGGGACAGTGCTCCCACTGCACATGCAT 360

Qy   361 CCTCAAGTGGCTGAATGCGCAGCAGGTTGCAGCAGCACTGCCCCATGTGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CCTCAAGTGGCTGAATGCGCAGCAGGTTGCAGCAGCACTGCCCCATGTGT 420

Qy   421 GAAGTTCAAAAGAGTGAAGCCCGTGCCGTGCCACTTCCCTCTCCTGTGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAAGTTCAAAAGAGTGAAGCCCGTGCCGTGCCACTTCCCTCTCCTGTGCT 480

Qy   481 AGCCCCTTCCCTCCCTCCCTCCCCAGATACAGCACCCCAAGTCCCCTCCC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGCCCCTTCCCTCCCTCCCTCCCCAGATACAGCACCCCAAGTCCCCTCCC 540

Qy   541 AGTGGTGCCCAGAGATCTCGGTCTGTCGCGGGGGACAAAGGATGCTTTCC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 AGTGGTGCCCAGAGATCTCGGTCTGTCGCGGGGGACAAAGGATGCTTTCC 600

Qy   601 CAAGGTTGAAAAGGAGACTTTGCTGACTGTTTTTGTTTTTCCCATCACAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CAAGGTTGAAAAGGAGACTTTGCTGACTGTTTTTGTTTTTCCCATCACAC 660

Qy   661 ATAAGTAAAACTCATTACAGTTCCAAGTTCGGATCCTGGGTCGACCTGCA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATAAGTAAAACTCATTACAGTTCCAAGTTCGGATCCTGGGTCGACCTGCA 720

Qy   721 TTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TTGAGTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATA 780